

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Campbell, Robert K.
Jameson, Bradford A.
Chappel, Scott C.
- (ii) TITLE OF INVENTION: HYBRID PROTEINS
- (iii) NUMBER OF SEQUENCES: 22
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BROWDY AND NEIMARK
 - (B) STREET: 419 Seventh Street N.W., Ste. 300
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 22207
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/011,936
 - (B) FILING DATE: 20 February 1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Browdy, Roger L.
 - (B) REGISTRATION NUMBER: 25,618
 - (C) REFERENCE/DOCKET NUMBER: CAMPBELL=2A
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202) 628-5197
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1049 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 278..1047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCCACATGGC TACAGGTAAG CGCCCCTAAATCCCTTTGG GCACAAATGTG TCCTGAGGGG	60
AGAGGCAGCG ACCTGTAGAT GGGACGGGGG CACTAACCCT CAGGTTTGGG GCTTCTCAAT	120
CTCACTATCG CCATGTAAGC CCAGTATTTG GCCAATCTCA GAAAGCTCCT CCTCCCTGGA	180
GGGATGGAGA GAGAAAAACA AACAGCTCCT GGAGCAGGGA GAGTGCTGGC CTCTTGCTCT	240
CCGGCTCCCT CTGTTGCCCT CTGGTTTCTC CCCAGGC TCC CGG ACG TCC CTG CTC	295
Ser Arg Thr Ser Leu Leu	
1 5	

CTG Leu	GCT Ala	TTT Phe	GGC Gly 10	CTG Leu	CTC Leu	TGC Cys	CTG Leu	CCC Pro 15	TGG Trp	CTT Leu	CAA Gln	GAG Glu	GGC Gly 20	AGT Ser	GCC Ala	343
GAT Asp	AGT Ser	GTG Val 25	TGT Cys	CCC Pro	CAA Gln	GGA Gly	AAA Lys 30	TAT Tyr	ATC Ile	CAC His	CCT Pro	CAA Gln 35	AAT Asn	AAT Asn	TCC Ser	391
ATT Ile	TGC Cys 40	TGT Cys	ACC Thr	AAG Lys	TGC Cys	CAC His 45	AAA Lys	GGA Gly	ACC Thr	TAC Tyr	TTG Leu 50	TAC Tyr	AAT Asn	GAC Asp	TGT Cys	439
CCA Pro 55	GGC Gly	CCG Pro	GGG Gly	CAG Gln	GAT Asp 60	ACG Thr	GAC Asp	TGC Cys	AGG Arg	GAG Glu 65	TGT Cys	GAG Glu	AGC Ser	GGC Gly	TCC Ser 70	487
TTC Phe	ACC Thr	GCT Ala	TCA Ser	GAA Glu 75	AAC Asn	CAC His	CTC Leu	AGA Arg	CAC His 80	TGC Cys	CTC Leu	AGC Ser	TGC Cys	TCC Ser 85	AAA Lys	535
TGC Cys	CGA Arg	AAG Lys	GAA Glu 90	ATG Met	GGT Gly	CAG Gln	GTG Val	GAG Glu 95	ATC Ile	TCT Ser	TCT Ser	TGC Cys	ACA Thr 100	GTG Val	GAC Asp	583
CGG Arg	GAC Asp	ACC Thr 105	GTG Val	TGT Cys	GGC Gly	TGC Cys	AGG Arg 110	AAG Lys	AAC Asn	CAG Gln	TAC Tyr	CGG Arg 115	CAT His	TAT Tyr	TGG Trp	631
AGT Ser	GAA Glu 120	AAC Asn	CTT Leu	TTC Phe	CAG Gln	TGC Cys 125	TTC Phe	AAT Asn	TGC Cys	AGC Ser	CTC Leu 130	TGC Cys	CTC Leu	AAT Asn	GGG Gly	679
ACC Thr 135	GTG Val	CAC His	CTC Leu	TCC Ser	TGC Cys 140	CAG Gln	GAG Glu	AAA Lys	CAG Gln	AAC Asn 145	ACC Thr	GTG Val	TGC Cys	ACC Thr	TGC Cys 150	727
CAT His	GCA Ala	GGT Gly	TTC Phe	TTT Phe 155	CTA Leu	AGA Arg	GAA Glu	AAC Asn	GAG Glu 160	TGT Cys	GTC Val	TCC Ser	TGT Cys	GCC Ala 165	GGT Gly	775
GCT Ala	GCC Ala	CCA Pro	GGT Gly 170	TGC Cys	CCA Pro	GAA Glu	TGC Cys	ACG Thr 175	CTA Leu	CAG Gln	GAA Glu	AAC Asn 180	CCA Pro	TTC Phe	TTC Phe	823
TCC Ser	CAG Gln	CCG Pro 185	GGT Gly	GCC Ala	CCA Pro	ATA Ile	CTT Leu 190	CAG Gln	TGC Cys	ATG Met	GGC Gly 195	TGC Cys	TGC Cys	TTC Phe	TCT Ser	871
AGA Arg	GCA Ala 200	TAT Tyr	CCC Pro	ACT Thr	CCA Pro	CTA Leu 205	AGG Arg	TCC Ser	AAG Lys	AAG Lys	ACG Thr 210	ATG Met	TTG Leu	GTC Val	CAA Gln	919
AAG Lys 215	AAC Asn	GTC Val	ACC Thr	TCA Ser	GAG Glu 220	TCC Ser	ACT Thr	TGC Cys	TGT Cys	GTA Val 225	GCT Ala	AAA Lys	TCA Ser	TAT Tyr	AAC Asn 230	967
AGG Arg	GTC Val	ACA Thr	GTC Val	ATG Met 235	GGG Gly	GGT Gly	TTC Phe	AAA Lys	GTG Val 240	GAG Glu	AAC Asn	CAC His	ACG Thr	GGG Gly 245	TGC Cys	1015
CAC His	TGC Cys	AGT Ser	ACT Thr 250	TGT Cys	TAT Tyr	TAT Tyr	CAC His	AAA Lys 255	TCT Ser	TA	AG					1049

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp
1 5 10 15
Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile
20 25 30
His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr
35 40 45
Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg
50 55 60
Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His
65 70 75 80
Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile
85 90 95
Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn
100 105 110
Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys
115 120 125
Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln
130 135 140
Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu
145 150 155 160
Cys Val Ser Cys Ala Gly Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu
165 170 175
Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys
180 185 190
Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys
195 200 205
Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys
210 215 220
Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val
225 230 235 240
Glu Asn His Thr Gly Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser
245 250 255

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 279..1199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCGAGATGG CTACAGGTAA GCGCCCCTAA AATCCCTTTG GGCACAATGT GTCCTGAGGG	60
GAGAGGTAGC GACCTGTAGA TGGGACGGGG GCACTAACCC TGAGGTTTGG GGCTTCTGAA	120
TGTGAGTATC GCCATGTAAG CCCAGTATTT GGCCAATGTC AGAAAGCTCC TGGTCCCTGG	180
AGGGATGGAG AGAGAAAAAC AAACAGCTCC TGGAGCAGGG AGAGTGCTGG CCTCTTGCTC	240
TCCGGCTCCC TCTGTTGCCC TGTGGTTTCT CCCCAGGC TCC CGG ACG TCC CTG	293
Ser Arg Thr Ser Leu	260
CTC CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT	341
Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser	265 270 275
GCC GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT	389
Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn	280 285 290
TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC	437
Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp	295 300 305
TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC	485
Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly	310 315 320 325
TCT TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC	533
Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser	330 335 340
AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG	581
Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val	345 350 355
GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT	629
Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr	360 365 370
TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT	677
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn	375 380 385
GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC	725
Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr	390 395 400 405
TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT GCT	773
Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ala	410 415 420
GGT GCT GGT CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG	821
Gly Ala Gly Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu	425 430 435
AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC	869
Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala	440 445 450

GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTC CCC GCC	917
Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala	
455 460 465	
CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC	965
Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile	
470 475 480 485	
CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCT	1013
Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala	
490 495 500	
GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC	1061
Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp	
505 510 515	
TGC GGG GGT CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCC CGC TTC	1109
Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Phe	
520 525 530	
CAG GAC TCC TCT TCC TCA AAG GCC CCT CCC CCC AGC CTT CCA AGC CCA	1157
Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro	
535 540 545	
TCC CGA CTC CCG GGG CCC TCG GAC ACC CCG ATC CTC CCA CAA TAA	1202
Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln	
550 555 560	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp	
1 5 10 15	
Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile	
20 25 30	
His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr	
35 40 45	
Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg	
50 55 60	
Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His	
65 70 75 80	
Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile	
85 90 95	
Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn	
100 105 110	
Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys	
115 120 125	
Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln	
130 135 140	

Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu
 145 150 155 160
 Cys Val Ser Cys Ala Gly Ala Gly Pro Arg Cys Arg Pro Ile Asn Ala
 165 170 175
 Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn
 180 185 190
 Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln
 195 200 205
 Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val
 210 215 220
 Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro
 225 230 235 240
 Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg
 245 250 255
 Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys
 260 265 270
 Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro
 275 280 285
 Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile
 290 295 300
 Leu Pro Gln
 305

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1147 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 278..1132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCGAGATGGC TACAGGTAAG CGCCCCCTAAA ATCCCTTTGG GCACAATGTG TCCTGAGGGG	60
AGAGGCAGCG ACCTGTAGAT GGGACGGGGG CACTAACCCT CAGGTTTGGG GCTTTTGAAT	120
GTGAGTATGG CCATGTAAGC CCAGTATTTG CCCAATCTCA GAAAGCTCCT GGTCCCTGGA	180
GGGATGGAGA GAGAAAAACA AACAGCTCCT GGAGCAGGGA CACTCCTGGC CTCTTGCTCT	240
GCGGCTCCGT GTGTTGCCCT GTGGTTTCTC CCCACGC TCC CGG ACG TCC CTG CTC	295
Ser Arg Thr Ser Leu Leu	310
CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC	343
Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala	
315 320 325	

GAT Asp 330	AGT Ser	GTG Val	TGT Cys	CCC Pro	CAA Gln 335	GGA Gly	AAA Lys	TAT Tyr	ATC Ile	CAC His 340	CCT Pro	CAA Gln	AAT Asn	AAT Asn	TCG Ser 345	391
ATT Ile	TGC Cys	TGT Cys	ACC Thr	AAG Lys 350	TGC Cys	CAC His	AAA Lys	GGA Gly	ACC Thr	TAC Tyr	TTG Leu	TAC Tyr	AAT Asn	GAC Asp 360	TGT Cys	439
CCA Pro	GGC Gly	CCG Pro	GGG Gly 365	CAG Gln	GAT Asp	ACC Thr	GAC Asp	TGC Cys	AGG Arg	GAG Glu	TGT Cys	GAG Glu	AGC Ser 375	GGC Gly	TCC Ser	487
TTC Phe	ACC Thr	GCT Ala 380	TCA Ser	GAA Glu	AAC Asn	CAC His	CTC Leu 385	AGA Arg	CAC His	TGC Cys	CTC Leu	AGC Ser 390	TGC Cys	TCC Ser	AAA Lys	535
TGC Cys	CGA Arg 395	AAG Lys	GAA Glu	ATG Met	GGT Gly	CAG Gln 400	GTG Val	GAG Glu	ATC Ile	TCT Ser	TCT Cys	TGC Cys	ACA Thr	GTG Val	GAC Asp	583
CGG Arg 410	GAC Asp	ACC Thr	GTG Val	TGT Cys	GGC Gly 415	TGC Cys	AGG Arg	AAG Lys	AAC Asn	CAG Gln 420	TAC Tyr	CGG Arg	CAT His	TAT Tyr	TGG Trp 425	631
AGT Ser	GAA Glu	AAC Asn	CTT Leu	TTC Phe 430	CAG Gln	TGC Cys	TTC Phe	AAT Asn	TGC Cys	ACC Thr	CTC Leu	TGC Cys	CTC Leu	AAT Asn 440	GGG Gly	679
ACC Thr	GTG Val	CAC His	CTC Leu 445	TCC Ser	TGT Cys	CAG Gln	GAG Glu	AAA Lys 450	CAG Gln	AAC Asn	ACC Thr	GTC Val	TGC Cys 455	ACC Thr	TGC Cys	727
CAT His	GCA Ala	GGT Gly 460	TTC Phe	TTT Phe	CTA Leu	AGA Arg	GAA Glu 465	AAC Asn	GAG Glu	TGT Cys	GTC Val	TCC Ser 470	TGT Cys	AGT Ser	AAC Asn	775
TGT Cys	AAG Lys 475	AAA Lys	AGC Ser	CTG Leu	GAG Glu	TGC Cys	ACG Thr	AAG Lys	TTG Leu	TCC Ser	CTA Leu	CCC Pro	CAG Gln	ATT Ile	GAG Glu	823
AAT Asn 490	GTT Val	AAG Lys	GGC Gly	ACT Thr	GAG Glu 495	GAC Asp	TCA Ser	GGC Gly	ACC Thr	ACA Thr 500	GCC Ala	GGT Gly	GCT Ala	GCC Ala	CCA Pro 505	871
GGT Gly	TGC Cys	CCA Pro	GAA Glu	TGC Cys 510	ACG Thr	CTA Leu	CAG Gln	GAA Glu	AAC Asn 515	CCA Pro	TTC Phe	TTC Phe	TCC Ser	CAG Gln 520	CCG Pro	919
GGT Gly	GCC Ala	CCA Pro	ATA Ile 525	CTT Leu	CAG Gln	TGC Cys	ATG Met	GGC Gly	TGC Cys	TGC Cys	TTC Phe	TCT Ser	AGA Arg 535	GCA Ala	TAT Tyr	967
CCC Pro	ACT Thr	CCA Pro 540	CTA Leu	AGG Arg	TCC Ser	AAG Lys	AAG Lys 545	ACG Thr	ATG Met	TTG Leu	GTC Val	CAA Gln 550	AAG Lys	AAC Asn	GTC Val	1015
ACC Thr	TCA Ser 555	GAG Glu	TCC Ser	ACT Thr	TGC Cys	TGT Cys	GTA Val	GCT Ala	AAA Lys	TCA Ser	TAT Tyr	AAC Asn	AGG Arg	GTC Val	ACA Thr	1063
GTA Val 570	ATG Met	GGG Gly	GGT Gly	TTC Phe	AAA Lys 575	GTG Val	GAG Glu	AAC Asn	CAC His	ACG Thr 580	GCG Ala	TGC Cys	CAC His	TGC Cys	AGT Ser 585	1111
ACT Thr	TGT Cys	TAT Tyr	TAT Tyr	CAC His 590	AAA Lys	TCT Ser	TAAGGATCCC TCGAG									1147

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp
1 5 10 15
Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile
20 25 30
His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr
35 40 45
Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg
50 55 60
Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His
65 70 75 80
Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile
85 90 95
Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn
100 105 110
Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys
115 120 125
Thr Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln
130 135 140
Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu
145 150 155 160
Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu
165 170 175
Ser Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
180 185 190
Thr Ala Gly Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu Gln Glu Asn
195 200 205
Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys
210 215 220
Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met
225 230 235 240
Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys
245 250 255
Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His
260 265 270
Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser
275 280 285

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 279..1287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTCGAGATGG CTACAGGTAA GCGCCCCTAA AATCCCTTTG GGCACAATGT GTCCTGAGGG	60
GAGAGGCAGC GACCTGTAGA TGGGACGGGG GCACTAACCC TCAGGTTTGG GGCTTCTGAA	120
TGTGAGTATC GCCATGTAAG CCCAGTATTT GGCCAATGTC AGAAAGCTCC TGGTCCCTGG	180
AGGGATGGAG AGAGAAAAAC AAACACCTCC TGGAGCAGGG AGAGTGCTGC CCTCTTGCTC	240
TCCGGCTCCC TCTGTTGCCC TCTGGTTTCT CCCCAGGC TCC CGG ACG TCC CTG	293
Ser Arg Thr Ser Leu	290
CTC CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT	341
Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser	305
GCC GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT	389
Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn	320
TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC	437
Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp	335
TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC	485
Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly	350
TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC	533
Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser	370
AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG	581
Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val	385
GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT	629
Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr	400
TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT	677
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn	415
GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC	725
Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr	430
TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT AGT	773
Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser	450

AAC TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT	821
Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile	
455 460 465	
GAG AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC ACA GCT GGT GCT GGT	869
Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Ala Gly Ala Gly	
470 475 480	
CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG AAG GAG GGC	917
Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu Lys Glu Gly	
485 490 495	
TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC GGC TAC TGC	965
Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys	
500 505 510	
CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC CTG CCT CAG	1013
Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala Leu Pro Gln	
515 520 525 530	
GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC CGG CTC CCT	1061
Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile Arg Leu Pro	
535 540 545	
GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC GTG GCT CTC	1109
Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala Val Ala Leu	
550 555 560	
AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC TGC GGG GGT	1157
Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly	
565 570 575	
CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCC CGC TTC CAG GAC TCC	1205
Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser	
580 585 590	
TCT TCC TCA AAG GCC CCT CCC CCC AGC CTT CCA AGC CCA TCC CGA CTC	1253
Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu	
595 600 605 610	
CCG GGG CCC TCG GAC ACC CCG ATC CTC CCA CAA T AAGGATCCCT CGAG	1301
Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln	
615 620	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp	
1 5 10 15	
Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile	
20 25 30	
His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr	
35 40 45	
Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg	
50 55 60	

Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His	65	70	75	80
Cys	Leu	Ser	Cys	Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile	85	90	95	
Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	100	105	110	
Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	115	120	125	
Ser	Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	130	135	140	
Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu	145	150	155	160
Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	Lys	Leu	165	170	175	
Cys	Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	Thr	Glu	Asp	Ser	Gly	Thr	180	185	190	
Thr	Ala	Gly	Ala	Gly	Pro	Arg	Cys	Arg	Pro	Ile	Asn	Ala	Thr	Leu	Ala	195	200	205	
Val	Glu	Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	Thr	Thr	Ile	210	215	220	
Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val	Leu	Gln	Gly	Val	Leu	225	230	235	240
Pro	Ala	Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg	Asp	Val	Arg	Phe	Glu	245	250	255	
Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val	Asn	Pro	Val	Val	Ser	260	265	270	
Tyr	Ala	Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu	Cys	Arg	Arg	Ser	Thr	275	280	285	
Thr	Asp	Cys	Gly	Gly	Pro	Lys	Asp	His	Pro	Leu	Thr	Cys	Asp	Asp	Pro	290	295	300	
Arg	Phe	Gln	Asp	Ser	Ser	Ser	Ser	Lys	Ala	Pro	Pro	Pro	Ser	Leu	Pro	305	310	315	320
Ser	Pro	Ser	Arg	Leu	Pro	Gly	Pro	Ser	Asp	Thr	Pro	Ile	Leu	Pro	Gln	325	330	335	

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Gly Ala Ala Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
Ala Gly Ala Gly
1

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTTCTCGAG ATGGCTACAG GTAAGCGCCC

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ACCTGGGGCA GCACCGGCAC AGGAGACACA CTCGTTTTTC

39

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGTGCCGGTG CTGCCCCAGG TTGCCCAGAA TGCACGCTAC AG

42

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTTGGATCC TTAAGATTTG TGATAATAAC AAGTAC 36

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCGTGGACCA GCACCAGCAC AGGAGACACA CTCGTTTTC 39

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGTGCTGGTG CTGGTCCACG GTGCCGCCCC ATCAAT 36

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTTTGGATCC TTATTGTGGG AGGATCGGGG TG 32

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTTAGATCT CTTCTTGCAC AGTGGAC 27

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGTGGTGCCT GAGTCCTCAG T

21

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ACTGAGGACT CAGGCACCAC AGCCGGTGCT GCCCCAGGTT G

41

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTTTTCTAGA GAAGCAGCAG CAGCCCATG

29

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTCCACAG CCAGGGTGGC ATTGATGGGG CGGCACCGTG GACCAGCACC AGCTGTGGTG

60

CCTGAGTCCT CAGTG

75